



Corrigendum

Corrigendum to “Solution structure and NMR characterization of the binding to methylated histone tails of the plant homeodomain finger of the tumour suppressor ING4” [FEBS Lett. 580 (2006) 6903–6908]

Alicia Palacios, Pascal Garcia, Daniel Padró, Eva López-Hernández, Irene Martín, Francisco J. Blanco *

NMR Group, Centro Nacional de Investigaciones Oncológicas (CNIO), Melchor Fernández Almagro 3, 28029 Madrid, Spain

The NMR structure calculated for the PHD domain of ING4, which was found to have flexible N- and C-termini, has been revised. The revised structure has been deposited with the Protein Data Bank. The published supplementary Table 1, which contains

the numerical statistics of the structure, should be replaced with a new table that corresponds to the actual deposited data in the PDB. The corrected supplementary table is given below.

Table 1

Statistics of the ensemble of 25 NMR structures of the ING4 PHD finger (Protein Data Bank entry 2K1J).

NOE distance constraints	
Intra-residual distances	258
Sequential distances	297
Medium-range distances ($i-j < 5$)	191
Long-range distances ($i-j \geq 5$)	329
Angular restraints	56
Total	1131
Final CYANA target function value ^a (\AA^2)	2.66
Maximum distance restraint violation (\AA)	0.39
Number of violations > 0.3	1
AMBER energy ^b (kcal/mol)	382.5
RMS deviations from ideal geometry	
Bond lengths (\AA)	0.01
Bond angles ($^\circ$)	2.28
RMSD to mean coordinates for residues 195–244 ^c (\AA)	
Backbone N,C α ,C'	0.27
All heavy atoms	1.19
Ramachandran plot statistics ^d	
Most favorable regions (%)	68.3
Additional allowed regions (%)	27.7
Generously allowed regions (%)	3.8
Disallowed regions (%)	0.2

^a The final CYANA [19] target function value was computed for the structure before energy minimization with AMBER [20].

^b Average values over the 25 final energy-minimized CYANA conformers.

^c The chain termini were found to be flexible and disordered in solution as described in detail in a later article [Palacios, A. et al. (2008) J. Biol. Chem. 283, 15956–15964].

^d Calculated with PROCHECK-NMR [Laskowski R.A., Rullmann, J.A.C., MacArthur, M.W., Kaptein, R. and Thornton, J.M. (1996) AQUA and PROCHECK-NMR: Programs for checking the quality of protein structures solved by NMR. J. Biomol. NMR 8, 477–486].

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* Corresponding author. Fax: +34 946572502.

E-mail address: fblanco@cicbiogune.es (F.J. Blanco).